

## II. REMARKS

Reconsideration and allowance of the present application based on the following remarks are respectfully requested. Entry of the foregoing amendment is respectfully requested pursuant to 37 C.F.R. §1.116 in that the applicants have complied with the examiner's suggestions made in the prior official action.

As a convenience to the examiner, attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached appendix is captioned **"Version with markings to show changes made"**.

The examiner objected to claims 17 and 18 for use of the language "nucleotides encoding a protein." In response, the applicants submit that this objection is now moot in that they have amended claims 17 and 18, herein, to adopt the examiner's suggestion. Therefore, the applicants request that the object to claims 17 and 18 be withdrawn.

The examiner rejected claims 24-26, 31, and 33 under 35 U.S.C. §112, second paragraph as allegedly being indefinite. The examiner alleged that the claims are confusing in that host cells and not vectors are made as biological deposits. With respect to claim 33, the examiner stated that the claim should be dependent from claim 32.

In response, the applicants have amended claims 24-26 to more clearly define applicants' claimed invention. Further, the applicants have canceled (without prejudice) claim 31. Finally, claim 33 has been amended to correctly depend from claim 32. In view of the foregoing, the applicants respectfully request that the rejection based upon 35 U.S.C. §112, second paragraph be withdrawn.

The examiner rejected claims 24-26, 31, and 33 under 35 U.S.C. §112, first paragraph in that the novel vector of the present specification, the enablement requirements of 35 U.S.C. §112, first paragraph must be satisfied.

In response, the applicants have enclosed herewith a "Declaration of Biological Deposit in Compliance with the Budapest Treaty," executed by the undersigned. Therefore, the applicants request that the rejection based upon 35 U.S.C. §112, first paragraph be withdrawn.

### III. CONCLUSION

All objections and rejections having been addressed, it is respectfully submitted that the present application is in a condition for allowance and a notice to that effect is earnestly solicited. If any point remains in issue which the examiner feels may be best resolved through a personal or telephone interview, the examiner is **strongly urged** to contact the undersigned at the telephone number indicated below.

Respectfully submitted,

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Enclosure: Appendix

APPENDIX

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS

The claims are amended as follows:

17. (Amended) An isolated DNA consisting essentially of [nucleotides] nucleotide sequences encoding a protein having the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, wherein said protein has transaldolase enzymatic activity.

18. (Amended) An isolated DNA consisting of [nucleotides] nucleotide sequences encoding a protein having the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, wherein said protein has transaldolase enzymatic activity.

24. (Amended) An isolated DNA encoding a protein having transaldolase enzymatic activity with an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or SEQ ID NO:4, and wherein said transaldolase enzymatic activity is essentially the same as that of the protein of SEQ ID NO:2 or SEQ ID NO:4 or the same as that of the protein encoded by pSUZ1 shown in figure 1 and as found in *Escherichia coli* JM109/pSUZ1 deposited under accession [deposition] number DSM 13263.

25. (Amended) An isolated DNA encoding a protein having transaldolase enzymatic activity with an amino acid sequence that is at least 90% identical to that of SEQ ID NO:2 or SEQ ID NO:4, and wherein said transaldolase enzymatic activity is essentially the same as that of the protein of SEQ ID NO:2 or SEQ ID NO:4 or the same as that of the protein encoded by pSUZ1 shown in figure 1 and as found in *Escherichia coli* JM109/pSUZ1 deposited under accession [deposition] number DSM 13263.

26. (Amended) An isolated DNA encoding a protein having transaldolase enzymatic activity with an amino acid sequence that is at least 95% identical to that of SEQ ID NO:2 or SEQ ID NO:4, and wherein said transaldolase enzymatic activity is essentially the same as that of the protein of SEQ ID NO:2 or SEQ ID NO:4 or the same as that of the

protein encoded by pSUZ1 shown in figure 1 and as found in *Escherichia coli* JM109/pSUZ1 deposited under accession [deposition] number DSM 13263.

31. Canceled

33. (Amended) The bacterium of claim [31] 32 wherein said bacterium is *Escherichia coli* JM109/pSUZ1 deposited under accession [Deposition] number DSM 13263.

End of Appendix

SEQ ID NO:2

LOCUS E13655 2260 bp DNA PAT 24-JUN-1998

DEFINITION gDNA encoding glucose-6-phosphate dehydrogenase.

ACCESSION E13655

VERSION E13655.1 GI:3252432

KEYWORDS JP 1997224661-A/1.

SOURCE Corynebacterium glutamicum.

ORGANISM Corynebacterium glutamicum

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
Actinomycetales; Corynebacterineae; Corynebacteriaceae;  
Corynebacterium.

REFERENCE 1 (bases 1 to 2260)

AUTHORS Hatakeyama,K., Kuwabara,K., Kobayashi,M. and Yugawa,H. .

TITLE GLUCOSE-6-PHOSPHATE DEHYDROGENASE AND DNA CAPABLE OF CODING THE  
SAME

JOURNAL Patent: JP 1997224661-A 1 02-SEP-1997;

MITSUBISHI CHEM CORP

COMMENT OS Brevibacterium flavum

PN JP 1997224661-A/1

PD 02-SEP-1997

PF 23-FEB-1996 JP 1996036345

PI HATAKEYAMA KAZUHISA, KUWABARA KOUICHIROU, KOBAYASHI MIKI, PI  
YUGAWA HIDEAKI

PC C12N9/04,C07H21/04,C12N15/09//C12N1/20,(C12N9/04,C12R1:13), PC  
(C12N1/20,

PC C12R1:13);

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

FH Key Location/Qualifiers

FH

FT source 1. .2260

FT /organism='Brevibacterium flavum' FT

/strain='MJ-233'

FT 5'UTR 1. .628

FT CDS 629. .2083

FT /product='glucose-6-phosphate dehydrogenase'.

FEATURES Location/Qualifiers

source 1. .2260

/organism='Corynebacterium glutamicum'

/db\_xref='taxon:1718'

BASE COUNT 512 a 659 c 592 g 497 t

ORIGIN

alignment\_scores:

Quality: 47.00 Length: 47  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-531-266-2 x E13655 ..

Align seg 1/1 to: E13655 from: 1 to: 2260

253 GlyAlaAsnThrGlnArgProLeuTrpAlaSerThrGlyValLysAsnPr 269  
|||||

106 GGCGCCAACACTCAGCGCCACTGTGGGCATCCACCGCGTGAAGAACCC 155  
|||||

269 oAlaTyrAlaAlaThrLeuTyrValSerGluLeuAlaGlyProAsnThrV 286  
|||||

156 TGCGTACGCTGCAACTCTTACGTTTCCGAGCTGGCTGGTCCAAACACCG 205  
|||||

286 alAsnThrMetProGluGlyThrIleAspAlaValLeuGlu 299  
|||||

206 TCAACACCATGCCAGAAGGCACCATCGACGCTGTTCTGGAA 246  
|||||

## SEQ ID NO:4

LOCUS E13655 2260 bp DNA PAT 24-JUN-1998

DEFINITION gDNA encoding glucose-6-phosphate dehydrogenase.

ACCESSION E13655

VERSION E13655.1 GI:3252432

KEYWORDS JP 1997224661-A/1.

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ORGANISM Corynebacterium glutamicum

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
Actinomycetales; Corynebacterineae; Corynebacteriaceae;  
Corynebacterium.

REFERENCE 1 (bases 1 to 2260)

AUTHORS Hatakeyama, K., Kuwabara, K., Kobayashi, M. and Yugawa, H. .

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SAME

JOURNAL Patent: JP 1997224661-A 1 02-SEP-1997;

MITSUBISHI CHEM CORP

COMMENT OS Brevibacterium flavum

PN JP 1997224661-A/1

PD 02-SEP-1997

PF 23-FEB-1996 JP 1996036345

PI HATAKEYAMA KAZUHISA, KUWABARA KOUICHIROU, KOBAYASHI MIKI, PI  
YUGAWA HIDEAKIPC C12N9/04,C07H21/04,C12N15/09//C12N1/20,(C12N9/04,C12R1:13), PC  
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PC C12R1:13);

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/strain='MJ-233'

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FT CDS 629. .2083

FT /product='glucose-6-phosphate dehydrogenase'.

FEATURES Location/Qualifiers

source

1. .2260

/organism='Corynebacterium glutamicum'

/db\_xref='taxon:1718'

BASE COUNT 512 a 659 c 592 g 497 t

ORIGIN

## alignment\_scores:

Quality: 47.00 Length: 47

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-531-266-4 x E13655 . . .

Align seg 1/1 to: E13655 from: 1 to: 2260

253 GlyAlaAsnThrGlnArgProLeuTrpAlaSerThrGlyValLysAsnPr 269

|||||

106 GGCGCCAACACTCAGCGCCACTGTGGGCATCCACCGCGTGAAGAACCC 155

269 oAlaTyrAlaAlaThrLeuTyrValSerGluLeuAlaGlyProAsnThrV 286

|||||

156 TGCCTACGCTGCAACTCTTTACGTTTCCGAGCTGGCTGGTCCAAACACCG 205

286 aAsnThrMetProGluGlyThrIleAspAlaValLeuGlu 299

|||||

206 TCAACACCATGCCAGAAGGCACCATCGACGCTGTCTGGAA 246